



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 02:22 PM GMT

PDB ID : 3X16
Title : Crystal structure of the catalase-peroxidase KatG W78F mutant from *Synechococcus elongatus* PCC7942
Authors : Tada, T.; Wada, K.; Kamachi, S.
Deposited on : 2014-10-30
Resolution : 2.65 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

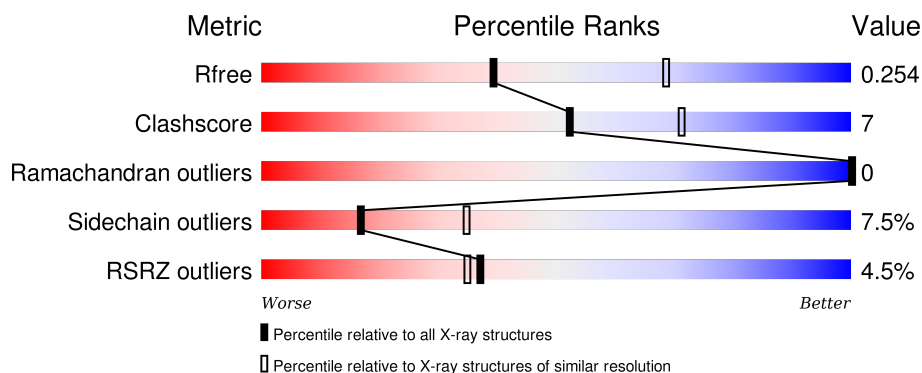
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.65 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	3152 (2.70-2.62)
Clashscore	102246	3524 (2.70-2.62)
Ramachandran outliers	100387	3469 (2.70-2.62)
Sidechain outliers	100360	3469 (2.70-2.62)
RSRZ outliers	91569	3161 (2.70-2.62)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	720	<div> <div>4%</div> <div>80%</div> <div>16%</div> <div>••</div> </div>

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

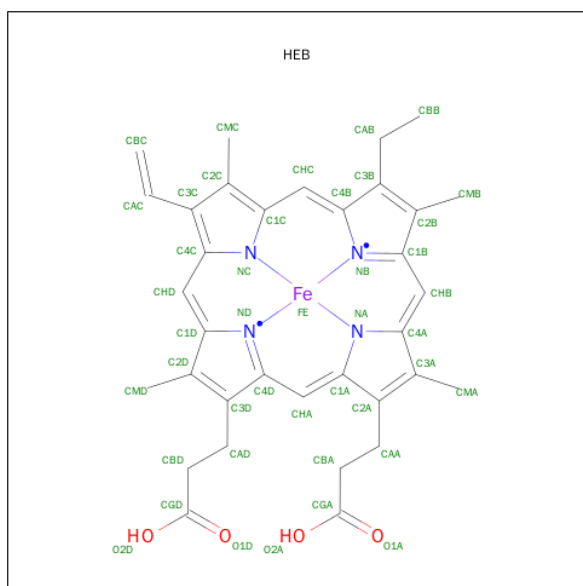
- Molecule 1 is a protein called Catalase-peroxidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	710	Total	C	N	O	S	0	0	0
			5579	3521	979	1060	19			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	78	PHE	TRP	ENGINEERED MUTATION	UNP Q31MN3

- Molecule 2 is HEME B/C (three-letter code: HEB) (formula: $\text{C}_{34}\text{H}_{34}\text{FeN}_4\text{O}_4$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0

- Molecule 3 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	3	Total 3	Na 3	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	155	Total 155	O 155	0	0

3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: Catalase-peroxidase



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	108.25Å 108.25Å 203.22Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	42.33 – 2.65 42.33 – 2.65	Depositor EDS
% Data completeness (in resolution range)	99.4 (42.33-2.65) 99.4 (42.33-2.65)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	6.39 (at 2.65Å)	Xtriage
Refinement program	REFMAC 5.7.0032	Depositor
R, R_{free}	0.197 , 0.254 0.201 , 0.254	Depositor DCC
R_{free} test set	1784 reflections (5.28%)	DCC
Wilson B-factor (Å ²)	45.0	Xtriage
Anisotropy	0.023	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 31.4	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.53$, $\langle L^2 \rangle = 0.37$	Xtriage
Outliers	1 of 35582 reflections (0.003%)	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	5780	wwPDB-VP
Average B, all atoms (Å ²)	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.42% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: NA, HEB

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.81	1/5725 (0.0%)	0.96	17/7796 (0.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	285	ASP	CB-CG	6.02	1.64	1.51

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	322	ASP	CB-CG-OD1	6.71	124.33	118.30
1	A	242	ARG	NE-CZ-NH1	6.63	123.62	120.30
1	A	362	ASP	CB-CG-OD1	6.63	124.27	118.30
1	A	385	ARG	NE-CZ-NH1	6.41	123.50	120.30
1	A	355	ASP	CB-CG-OD2	-6.14	112.78	118.30
1	A	673	ARG	NE-CZ-NH1	6.11	123.36	120.30
1	A	327	ARG	NE-CZ-NH2	-6.07	117.26	120.30
1	A	424	ASP	CB-CG-OD1	-5.91	112.98	118.30
1	A	370	VAL	CB-CA-C	-5.75	100.47	111.40
1	A	362	ASP	CB-CG-OD2	-5.72	113.15	118.30
1	A	502	ARG	NE-CZ-NH2	-5.70	117.45	120.30
1	A	310	LEU	CB-CG-CD2	5.63	120.58	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	404	ARG	NE-CZ-NH1	5.46	123.03	120.30
1	A	352	ARG	NE-CZ-NH2	-5.35	117.63	120.30
1	A	385	ARG	NE-CZ-NH2	-5.31	117.64	120.30
1	A	394	ASP	CB-CG-OD1	5.23	123.01	118.30
1	A	593	ASP	CB-CG-OD1	5.09	122.88	118.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	15	ALA	Peptide
1	A	210	GLU	Peptide

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	5579	0	5363	73	0
2	A	43	0	32	2	0
3	A	3	0	0	0	0
4	A	155	0	0	6	0
All	All	5780	0	5395	74	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 7.

All (74) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:94:TRP:CH2	1:A:222:TYR:HE2	1.25	1.54
1:A:222:TYR:HE1	1:A:248:MET:SD	1.31	1.49
1:A:222:TYR:CE1	1:A:248:MET:SD	2.07	1.46
1:A:94:TRP:CH2	1:A:222:TYR:CE2	2.15	1.31
1:A:94:TRP:HH2	1:A:222:TYR:CE2	1.48	1.27
1:A:94:TRP:CZ2	1:A:222:TYR:HE2	1.84	0.95

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:114:GLN:HE21	1:A:132:ARG:HH11	1.27	0.80
1:A:222:TYR:CZ	1:A:248:MET:SD	2.75	0.79
1:A:94:TRP:CZ2	1:A:222:TYR:CE2	2.67	0.78
1:A:618:ASN:HB3	1:A:622:THR:HG22	1.69	0.74
1:A:648:LEU:C	1:A:648:LEU:HD12	2.13	0.69
1:A:38:HIS:H	1:A:179:HIS:HE1	1.43	0.66
1:A:385:ARG:NH2	1:A:389:GLU:OE1	2.29	0.65
1:A:595:THR:HG21	1:A:605:MET:SD	2.38	0.64
1:A:171:ALA:H	1:A:411:HIS:HE1	1.48	0.61
1:A:639:PHE:O	1:A:643:THR:HB	2.02	0.60
1:A:103:ALA:HA	1:A:567:VAL:HG22	1.84	0.60
1:A:320:GLN:HB2	4:A:953:HOH:O	2.02	0.59
1:A:114:GLN:HE21	1:A:132:ARG:NH1	1.98	0.59
1:A:106:ARG:HH21	1:A:596:GLN:HE21	1.51	0.59
1:A:618:ASN:CB	1:A:622:THR:HG22	2.33	0.58
1:A:251:ASN:C	1:A:251:ASN:HD22	2.09	0.56
1:A:488:ARG:O	1:A:493:LYS:HD3	2.06	0.56
1:A:99:THR:HG22	1:A:107:GLY:HA3	1.88	0.56
1:A:502:ARG:O	1:A:506:VAL:HG23	2.05	0.55
1:A:544:ILE:HG22	4:A:1020:HOH:O	2.05	0.55
1:A:428:GLU:HB2	4:A:949:HOH:O	2.07	0.55
1:A:237:THR:O	1:A:238:ALA:C	2.44	0.55
1:A:99:THR:HG22	1:A:107:GLY:CA	2.38	0.54
1:A:94:TRP:CD1	1:A:95:HIS:HD2	2.27	0.53
1:A:179:HIS:HD2	1:A:180:PRO:O	1.93	0.52
1:A:509:VAL:O	1:A:513:ILE:HD12	2.09	0.52
1:A:216:VAL:HG23	1:A:217:THR:HG22	1.93	0.51
1:A:38:HIS:H	1:A:179:HIS:CE1	2.26	0.50
1:A:488:ARG:NH2	1:A:554:ASP:HB3	2.27	0.49
1:A:66:ASP:OD2	1:A:141:LYS:NZ	2.44	0.49
1:A:591:LEU:O	1:A:595:THR:HG23	2.12	0.49
1:A:588:GLU:OE2	1:A:673:ARG:NH2	2.45	0.49
1:A:628:THR:HB	1:A:630:ARG:H	1.79	0.48
1:A:112:GLY:O	1:A:115:ARG:HG2	2.14	0.48
1:A:468:ASP:OD2	1:A:576:ARG:NH1	2.47	0.47
1:A:412:ARG:NH2	1:A:479:ARG:HD2	2.29	0.47
2:A:801:HEB:HMC1	2:A:801:HEB:HBC1	1.97	0.47
1:A:25:TRP:HB2	1:A:26:TRP:CE3	2.50	0.46
1:A:202:ARG:HD3	1:A:209:LEU:HD11	1.97	0.46
1:A:94:TRP:CH2	1:A:222:TYR:CZ	2.95	0.45
1:A:136:TRP:N	1:A:137:PRO:CD	2.78	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:251:ASN:ND2	1:A:254:GLU:H	2.14	0.45
1:A:628:THR:HG22	1:A:637:ASP:OD2	2.17	0.44
1:A:127:ASN:HA	1:A:129:ASP:OD1	2.17	0.44
1:A:224:ASN:HB3	1:A:227:GLY:O	2.18	0.44
1:A:602:ALA:HB3	1:A:603:PRO:HD3	2.00	0.43
1:A:126:THR:O	1:A:127:ASN:HB2	2.18	0.43
1:A:120:ASN:HD21	1:A:282:GLU:HG2	1.83	0.43
1:A:113:ASN:HD22	1:A:114:GLN:N	2.17	0.43
1:A:317:HIS:HD2	4:A:916:HOH:O	2.02	0.43
1:A:34:ILE:HD11	1:A:592:LEU:HG	2.01	0.43
1:A:381:ASP:HB3	1:A:384:TYR:HB2	2.01	0.42
1:A:94:TRP:CD1	1:A:95:HIS:CD2	3.07	0.42
1:A:618:ASN:ND2	4:A:1055:HOH:O	2.52	0.42
1:A:80:ALA:HB2	1:A:85:TYR:CE1	2.55	0.42
1:A:258:LEU:HB3	2:A:801:HEB:HMC1	2.01	0.41
1:A:317:HIS:CD2	4:A:916:HOH:O	2.73	0.41
1:A:251:ASN:HD21	1:A:254:GLU:H	1.69	0.41
1:A:499:GLU:OE1	1:A:576:ARG:NH2	2.54	0.41
1:A:95:HIS:ND1	1:A:125:ASN:ND2	2.68	0.41
1:A:80:ALA:HB2	1:A:85:TYR:CD1	2.56	0.41
1:A:28:LYS:HD3	1:A:28:LYS:H	1.86	0.40
1:A:413:ASP:HA	1:A:477:ASP:HB2	2.03	0.40
1:A:99:THR:HG23	1:A:186:TRP:CH2	2.57	0.40
1:A:701:VAL:O	1:A:702:ARG:C	2.58	0.40
1:A:715:ASP:C	1:A:715:ASP:OD1	2.59	0.40
1:A:591:LEU:O	1:A:595:THR:CG2	2.69	0.40
1:A:437:PRO:O	1:A:553:GLY:HA3	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	708/720 (98%)	670 (95%)	38 (5%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	573/581 (99%)	530 (92%)	43 (8%)	17	35

All (43) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	16	THR
1	A	22	THR
1	A	24	GLU
1	A	28	LYS
1	A	31	ASN
1	A	32	LEU
1	A	40	ARG
1	A	68	GLN
1	A	92	LEU
1	A	113	ASN
1	A	120	ASN
1	A	124	ASP
1	A	154	TYR
1	A	165	LEU
1	A	191	GLU
1	A	198	ASN
1	A	204	THR
1	A	206	ASP
1	A	217	THR
1	A	224	ASN
1	A	242	ARG
1	A	251	ASN
1	A	310	LEU

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Mol	Chain	Res	Type
1	A	333	ASP
1	A	359	ASP
1	A	370	VAL
1	A	373	ASP
1	A	427	GLN
1	A	442	ASN
1	A	511	GLU
1	A	527	LEU
1	A	544	ILE
1	A	567	VAL
1	A	582	ASP
1	A	595	THR
1	A	607	VAL
1	A	608	LEU
1	A	622	THR
1	A	628	THR
1	A	643	THR
1	A	656	LEU
1	A	663	LYS
1	A	719	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	31	ASN
1	A	37	GLN
1	A	68	GLN
1	A	113	ASN
1	A	114	GLN
1	A	120	ASN
1	A	125	ASN
1	A	179	HIS
1	A	224	ASN
1	A	251	ASN
1	A	317	HIS
1	A	411	HIS
1	A	440	ASN
1	A	446	GLN
1	A	535	GLN
1	A	572	HIS
1	A	596	GLN
1	A	655	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 4 ligands modelled in this entry, 3 are monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	HEB	A	801	1	24,50,50	2.15	11 (45%)	20,82,82	3.01	12 (60%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	HEB	A	801	1	-	0/8/54/54	0/0/8/8

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	801	HEB	C4B-NB	-3.87	1.31	1.36
2	A	801	HEB	C4C-NC	-3.50	1.32	1.36
2	A	801	HEB	C4D-ND	-3.23	1.32	1.36
2	A	801	HEB	CAB-C3B	-2.25	1.48	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	801	HEB	CAA-C2A	-2.07	1.48	1.52
2	A	801	HEB	C1A-CHA	2.12	1.45	1.39
2	A	801	HEB	C3B-C2B	2.44	1.44	1.37
2	A	801	HEB	C4A-CHB	2.46	1.46	1.39
2	A	801	HEB	C3D-C2D	2.56	1.45	1.37
2	A	801	HEB	C2A-C3A	3.08	1.46	1.37
2	A	801	HEB	C3C-C2C	4.33	1.46	1.40

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	801	HEB	CAA-CBA-CGA	-3.26	106.77	112.75
2	A	801	HEB	CBB-CAB-C3B	-2.46	107.22	112.21
2	A	801	HEB	CAD-CBD-CGD	-2.21	108.70	112.75
2	A	801	HEB	CAD-C3D-C2D	-2.17	122.80	129.00
2	A	801	HEB	CMC-C2C-C1C	-2.03	125.01	128.36
2	A	801	HEB	CMB-C2B-C3B	2.01	129.44	125.24
2	A	801	HEB	C3C-C4C-NC	2.04	114.80	110.94
2	A	801	HEB	CAB-C3B-C4B	2.31	130.90	127.18
2	A	801	HEB	CMA-C3A-C2A	3.95	133.50	125.24
2	A	801	HEB	CBD-CAD-C3D	4.48	120.56	112.53
2	A	801	HEB	CMC-C2C-C3C	4.70	134.29	125.09
2	A	801	HEB	CAD-C3D-C4D	8.54	136.28	127.01

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	801	HEB	2	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	710/720 (98%)	-0.03	32 (4%) 37 35	31, 46, 74, 119	0

All (32) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	199	PRO	6.4
1	A	206	ASP	6.0
1	A	200	ASN	6.0
1	A	204	THR	5.0
1	A	23	ALA	4.3
1	A	24	GLU	4.1
1	A	192	TRP	3.8
1	A	198	ASN	3.5
1	A	203	TYR	3.4
1	A	190	LYS	3.1
1	A	19	ASN	3.1
1	A	442	ASN	3.0
1	A	195	PRO	2.9
1	A	208	GLU	2.8
1	A	18	VAL	2.8
1	A	25	TRP	2.7
1	A	48	ASP	2.6
1	A	191	GLU	2.6
1	A	207	ARG	2.5
1	A	197	THR	2.5
1	A	543	GLU	2.4
1	A	201	SER	2.3
1	A	720	ASP	2.3
1	A	443	TYR	2.3
1	A	194	PRO	2.2
1	A	516	ALA	2.1
1	A	205	GLY	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	28	LYS	2.0
1	A	211	ASN	2.0
1	A	53	GLU	2.0
1	A	193	VAL	2.0
1	A	429	ASP	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q < 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
2	HEB	A	801	43/43	0.97	0.19	0.59	27,35,40,42	0
3	NA	A	803	1/1	0.70	0.13	-0.71	40,40,40,40	0
3	NA	A	802	1/1	0.96	0.05	-2.34	38,38,38,38	0
3	NA	A	804	1/1	0.96	0.10	-	49,49,49,49	0

6.5 Other polymers [i](#)

There are no such residues in this entry.